



Blast 2 Sequences results

PubMed

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Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

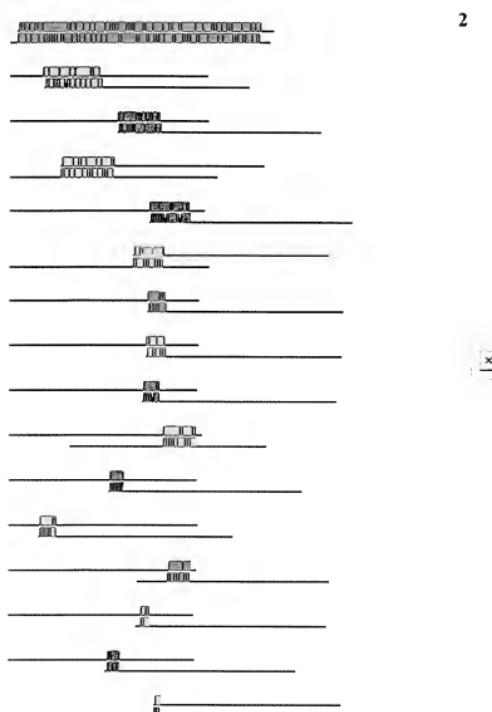
Matrix **BLOSUM62** gap open:**11** gap extension:**1**x_dropoff: **0** expect: **10.0000** wordsize: **3** Filter View option **Standard**Masking character option **X** for protein, **n** for nucleotide Masking color option **Black** Show CDS translation Align**Sequence 1:** gi|126012562|low density lipoprotein-related protein_1 [Homo sapiens]

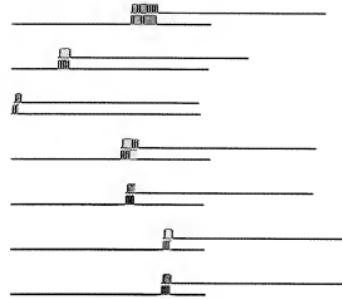
Length = 4544 (1 .. 4544)

Sequence 2: gi|126012573|low density lipoprotein-related protein_2 [Homo sapiens]

>gi|160332309|sp|P98164.3|LRP2_HUMAN Low-density lipoprotein receptor-related protein 2 precursor (Megalin) (Glycoprotein 330) (gp330)

Length = 4655 (1 .. 4655)





1

NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 2605 bits (6751), Expect = 0.0
 Identities = 1626/4335 (37%), Positives = 2311/4335 (53%), Gaps = 270/4335 (6%)

Query 26	TCSPKQFACRDQITCISKWRCRDGERDCPDGSDEAPEI	CQSQAQRCQPNEHNCLGTEL	85
Sbjct 221	TCGGYQTCPMSG-RCIYQNWVCDGEDDCKDNGDEDG	CESPHDVHKCSPREWCPESGRC	279
Query 86	VPMRLCNGVQDCMDGSDE	-GPHCRELQQNCNSRLGCQHHCVPTLDGPTCYCNSSFQ	140
Sbjct 280	++ +C+G+ DC DE G +C CS L C+C T G C+C +	ISIYKVCDGILDCPGRDENNTNSTGKYSMTL--CSALNCNQYQCHETPYGGACFCPPGYI	337
Query 141	LQA-DGKTCDFDECSCVYGTCSQLCTNDGSFICGCGVEGYLLQPDNRSCAKNEPVDRPP	+ +TC +FD+C ++G C Q C + G +C C EGY+L+ + CKA + +	199
Sbjct 338	INHNDSRTCVEFDDCQIWIWICDQKCESRPGHLCHCEEGYILER-GQYCKANDSFGEAS-	INHNSRTCVEFDDCQIWIWICDQKCESRPGHLCHCEEGYILER-GQYCKANDSFGEAS-	395
Query 200	VLLIANSQNILATYLSGAQVSTITPTSTRQTTA-MDFSYANETVCWVHVGDSAATQLKC	++ +N +++L + G + + R + F Y + V W Q ++	258
Sbjct 396	-IIFSNGRDILLIGDIHGRSFRILVESQNRGVAVGVAFHYHQLQRFWT---DTVQNKVFS	-IIFSNGRDILLIGDIHGRSFRILVESQNRGVAVGVAFHYHQLQRFWT---DTVQNKVFS	450
Query 259	ARMPGLKGFDDEHTINISLSLHHVEQMAIDWLGTGNFYFVDDIDDRIFVCNRNGDTCVTLL	+ GL + +N+S+ E +A+DW+ Y V+ +RI + N +G VTL+	318
Sbjct 451	VINGLN---IQEVLNVSVETP---ENLAVWDVNKNYLVETKVNRIIDMVNLGDSYRVTLI	VINGLN---IQEVLNVSVETP---ENLAVWDVNKNYLVETKVNRIIDMVNLGDSYRVTLI	505
Query 319	DLELYNPKGIALDPAMGKVFFTDYQGI--PKVERCDMDGQNRTKLVDISKIVFPFHGITLD	L +P+GIA+D+ +G +FF+D+ + PK+ER MDG NR LV +K+ +P G+TLD	375
Sbjct 506	TENLGHPRGIAVDPTVGYLFFSDWESLSGEPKLERAFMDGSNRKDVLTKTLGWPGVTLD	TENLGHPRGIAVDPTVGYLFFSDWESLSGEPKLERAFMDGSNRKDVLTKTLGWPGVTLD	565
Query 376	LVSRLVWYDAYLDYIEVVVDYEGKGRQTIIQG-ILIEHLYGLTVFENLYATNSNDANAQ	++S+ VYW D+ DYIE V Y+G R+T++ G LI H +G+++FE ++ T+	434
Sbjct 566	MISKRVYWWDSRFDYIETVTDGIIQRKTVVHGGSLIPHPPGVSLFEGQVFTTD-----W	MISKRVYWWDSRFDYIETVTDGIIQRKTVVHGGSLIPHPPGVSLFEGQVFTTD-----W	619
Query 435	QKTSVIRVNRFNSTEYQVVTTRVD-KGGALHIYHQRRQPRVRSHACENDQYGKPGGCSDIC	K +V++ N+F+ T QV + + + +YH RQP + +N+ GGC +C	493
Sbjct 620	TKMAVLKANKFTETNPQVYYQQASLRPYGVTVYHSLRQPYATNPCKDNN----GGCEQVC	TKMAVLKANKFTETNPQVYYQQASLRPYGVTVYHSLRQPYATNPCKDNN----GGCEQVC	674
Query 494	LLA---NSHKARTCRCSRSGFSLGSDGKSKKPEHEFLVYKGKRPGIIRGMDMGA	KVPD +L+ N C+C GF L +D + C ++ FL+ IRG+ +	549
Sbjct 675	VLSHRTDNDGLGRFKRCTFGQLDTERHCIAVQN--FLIFSS--QVAIRGIPFTLSTQE	VLSHRTDNDGLGRFKRCTFGQLDTERHCIAVQN--FLIFSS--QVAIRGIPFTLSTQE	730

Blast Results

Query	550	EHHIPIENLMNPR---ALDFHAETGFYFADTTSYLIGRQKIDGTERETILKGDIHNVEG + M+P+ NP +DF A+ I+F+D + ++I +QKIDGT RE + + + NVE	606
Sbjct	731	DVMVPVSG--NPSFFVGIDFDAQDSTIFFSDMSKHMIFKQKIDGTTREILAAVRVENVES	788
Query	607	VAVDWMDGMNLWYTDGGPKKTISVARLEKAAQTRKTLIEGKMTHPRAIVVDPLNGWMYWT +A DW+ NLYWTD K+ISV RL A +TR+T++ + +PR+VV P G+++TD	666
Sbjct	789	LAFDWISKNLYWTDASH-YKSISVMRL--ADKTRRTVHQ-YLNPNRSVVVHPFAGYLFTTD	844
Query	667	WEEDPKDSRRGLERAWMDGSHRDIFVTSTSITVLWPNGSLSDIPAGRLYWVDAFYDRIETI W R ++ RAW DGSH V + T+ WPNGL+D A RLYNVA+D+IE	726
Sbjct	845	W-----FRPAKIMRAWSDGSHL-LPVINTTLGWPNGLAIDWAASRLYWDAYFDKIEHS	897
Query	727	LLNGBTDRKIVYEGPELNHAFGLCHHNGQFLWFTTEYRSGSVYRLERGVGGAPPTVTLRSER +G DR+ + + H FGL G +LF+T+R G++ R+ + GG +T+RS	786
Sbjct	898	TFDGLDERRLGHIEQMTHPTFGLAIFGSHLFTDWRLAGIIRVRKADGGE---MTVIRSGI	954
Query	787	PPIFEIRMYDAQQQVQVTNKCVRN---NGGCSSLCLATPG-SRQCACAEQVLDAGVTC I ++ YD Q G+N C NG CS C P R C C L ++ +TC	842
Sbjct	955	AYILHLKSYDVNIQ-TGSNACNQPTHNGDCSHFCFPVPNFQRVCGCPYGMRLASNHTC	1013
Query	843	LANPSVYPPP-QCQPGEFACANSRCIQRERWKCDGNDNCLDNSDEAPALCHQHCTPSDRFK +P+ PP QC F C N RC+ + CDG +DC DNSDE +TC S F	901
Sbjct	1014	EGDPTNEPPTEQCGLFSPPCKNGRCVPNYYLCDGVDCHDNDEQLCGTLNNNTCSSSAFT	1073
Query	902	CENNRCIPRNWLCDGNDNCNSDEDSNA-TCSARTCPNPQFSCASGRCIPIWSLCDLDD C + CIP W CD NDC + DE N T + +C Q+C + +CI +W CD D+D	960
Sbjct	1074	CGHGECAPIAHWRCDKRNDCVGDGSDHEHNCPTTHAPASCLDTQYTCNDNHQC1SKNWVCDTDND	1133
Query	961	CGDRSDESASCAYPTCFPLTQFTCNNGRCININWRCDDNDNDCGDNDEAGCSHCSSTQF CGD SDE + TC P +QF C N RC1++++ CD D DC D SDE GC +C+++QF	1020
Sbjct	1134	CGDGSDEKNCNSTETCQP-SQFNCPNHRICIDLSFVCDGDKDCVGDGSDEVGCVLNCTASQF	1192
Query	1021	KCNSG-RCIPEHWTCDGNDCGDYSDETHANCTNQATRPPGCHTDEFQCRLDGLCIPLR KC SG +CI CDP DC D SDE A C TRPPG CH+DEFQ+ DG+CIP	1079
Sbjct	1193	KCASGDKCIGVTNRCDDGVDCSDNSDE--AGCP---TRPPGMCHSDEFQCQEDGICIPNF	1247
Query	1080	WRCDGDTDCMDSSDEKESEGVTHVCDPSVKFGCKDSARCISKAWCDDGNDNCDNSDEEN W CDG DC+ SDE + V C PS F C D+ CI +AW+CD DNDC D SDE++	1139
Sbjct	1248	WECGDHPDCLYGSDEHNA-CVPKTC-PSSYFHC-DNGNCIIRAWLCDRDNDCGMSDEKD	1304
Query	1140	CESLACRPPSHP---CANNNTSVCCLPDPDKLCDGNDNDCGDSDEGEELCDQCSLNNNGCOSHNC C + R PS +N V L + G + CS NGG+C H C	1196
Sbjct	1305	CPTQPFRCPSWQWQCLGHNICVNLSVVCDFGIFDCPNGTDDESPLCNGNSCSDFNGGCTHEC	1364
Query	1197	SVAPGEGIYCSCPLGMLGPNDHTCQIQSYYCAHKLCSQSQCDQNPKFSVKCSCYEGWLEP P G C CPLG L D+ TC+ C CSQ C + S +CSC G+LE	1256
Sbjct	1365	VQEFP-GAKCLCPLGFLANDSKTEDIDECDILGSCSQHCYNMRGSRCSCTGYMLES	1423
Query	1257	DGESCRSLDPFPKFPIIFSNRHEIRRDLHKGDYSV---LVPGLRNTIALDFHLSQSALYWT DG +C+ ++ +++++I + +++ LV +A+DF ++W+	1314
Sbjct	1424	DGRTCKVTAESLLLVLASQNKIIADSVTQSVHNIIYSLVENGSYIVAVDPDISGRIFWS	1483
Query	1315	DVVEDK1YRGKLDDNGALTSFEVVIQYGLATPEGLAVIDWAGNIYWVESNLNDQIEVAKLD D + K + NG T VV + E + A+DW+ N+YW + L+ IEV+K+D	1374
Sbjct	1484	DATQGKWTSA--FQNG---TDRRWFDSIIILTETIAIDWVGRNLWTDYALETIEVSKID	1539
Query	1375	GTLRTTLLLAGDIEHPRAIALDPR---DGILFWTDWDASLPRIEAAASMAGGRRTVHRETGS G+ RT L++ ++ +PR +ALDPR + +LFW+DW PRIE ASM G+ R + ++	1432
Sbjct	1540	GSHRTVTLISKNLTNPRGLALDPRMNEHLLFWSDWGHH-PRIERASMDGSMRTVIVQDKIF	1598
Query	1433	GGWPNGLTVDYLEKRILWIDARSDAIYSARYDGSGSHMEVLRGHEFLSHPFAVTLYGGEVY WP GLT+DY + + +D+ D + Y+G +V+ + HP+A+TL+ VY	1492
Sbjct	1599	--WPCGLTIDYPNRLLYFMDSYLDYMFCDYNGHHRQVIAISDLIIRHPYATLTFEDSVY	1656

Query	1493	WTDWRNTTLAKANKWTGHNVTVQRTNTQPFDLQVYHPSRQPMAPNPCEANGQQGPCSHL	1552
	WTD T + +ANKW G N +VV P + HPS+QP + NPC + CSHL		
Sbjct	1657	WTDRATRRVMRANKWHGGNQSVMYNIQWPGLIVAVHPSKQPNVPCAFSR---CSHL	1712
Query	1553	CLINYN--RTVSCACPHMLKMHKDNTTCY-EFKKFLLYARQMEIRGVLDAPYYNYIISF	1609
	CL++ SC CP L D C ++ FL+ RQ I G+ L+ +		
Sbjct	1713	CLLSSQGPHFYSCVCPGSWSLSPDPLLNLCRDDQPFLITVRQHIIIFGISLNPEVKSNDAMV	1772
Query	1610	TPVDIDNVTVLDYDAREQRVYWSDVRTQAIKRAFINGTGVETVVSADLPN-AHGLAVDWV	1668
	+ I N ++++D EQ +YW + I R +GT S + + LA+DW+		
Sbjct	1773	PIAGIQNGLDVEFDDAEQYIYWE-NPGEIHRVKTDGTNRRTVFASISMVGPSMNLALDWI	1831
Query	1669	SRNLFWTSYDTNKKQINVARLDGSFKNAVVQ-----GLEQPHGLVVHPLRGKLYWTGDG	1722
	SRNL+ T+ T ++ D ++ + + G+ P G+ V P RGKLYW+D		
Sbjct	1832	SRNLYSTNPRTQSIETVLTLHGDIRYRKTLLANDGTALGVGFPIGITVDPARGKLYWSDQG	1891
Query	1723	N-----ISMANMDGSNRNLLFGSQGKPGV-LAIDFPESKLYWISSGNHTINRCNLDGS	1774
	I+ ANMDG++ LF+G + + + D E KLYW +G I R N+DG+		
Sbjct	1892	TDSGPVAKIASANMDGTSVKTFLFTGNLEHLCVTLIDIEBKLYWAVTGRGVIERGNVDGT	1951
Query	1775	GLEVIDAMRSQLGKATALAIMGDKLWWADQVSEKMGTCISKADGGSVSVLRNSTLVMHMK	1834
	++ QL +A+ L++ D+ E + KA G+ +VLR++ + ++		
Sbjct	1952	DRMILV---HQLSHPWGIAVHDSDLFLYTYTDEQEYEVIERVDKATGANKIVLRLDNVPNLRGLQ	2008
Query	1835	VYDESIQLDHKGKTNPCSVNNGDCSQLCLPTSETTRSCMCATAGYSLRSGQQACEGVGSFLL	1894
	VY + + N CS N C Q+CLP SC C G+ L + +C SF++		
Sbjct	2009	VYHPRNAE--SSNGCSNNNMNAQCQICLPPVGGFLSCACATGFKLNPDNRSCSPYNSFIV	2066
Query	1895	YSVHEGIRGIPLDPNKSDALVPVSGTSL-AVGIDFHAEENDTIYWDGMGSTIS----R	1948
	S+ IRG L+ +D S+ +VPV+G A+ +D + IYW D S S R		
Sbjct	2067	VSMLSAIRGFSLELDSDHSETMPVAGQGRNALHVDVDVSSGFIYWCDFSSSVASDNAIRR	2126
Query	1949	AKRDQTWRDVTVNTGIGR--VEGIAVDWIAGNIYWTDQGFD--VIEVARLNGSFRYVVIS	2004
	K D + ++VT+GIG V GIAVDW+AGN+Y+T+ +IEV R+N ++R V++		
Sbjct	2127	IKPDGSSLMNIVTHGIGENGVRGIAVDWVAGNLYFTNAFVSETLIEVLRINTTYRRVLLK	2186
Query	2005	QGLDKPRAITVHPEKGYLFWTEWGQYPRIERSRLDGTERVVLVNVNISWPNGSIVDQDG	2064
	+D PR I V P+ YLFW ++GQ P+IERS LD T R VLV+ I P G++VD DG		
Sbjct	2187	VTVDMPRHIVVDPKNRVFLWADYQGRPKIERSFLDCTNRTLVSEGIVTPRGLAVDRSDG	2246
Query	2065	KLYWCDARTDKIERIDLETGENREVR--LSSNNMDMFSVSVFEDFIYWSDRTHANGSIKRG	2123
	+YW D D I RI + GEN EV+ S + ++VPE+ I W DR		
Sbjct	2247	YVYVWVDSLIDIIARIRIN-GENSEVIRGSRYPTPYGITVFFENSIIWVDRNLKKIFQASK	2305
Query	2124	SKDNATDSVPLRTGIGVQLKDIKVFNDRQK-----GTVCAVANGGCQQCL-YRGRG	2176
	+N +R I L+D+ +F++ Q N C NGGC LC G		
Sbjct	2306	EPENTEPPTVIRDNIN-WLRTDTIFDKQVQPRSPAEVNNNPCLENNNGCSSLFCALPGLH	2364
Query	2177	QRACACAHGMLAEDGASCR-EYAGYLAYSERTILKSIHSLSDERNLNAPVQPFEDPEHMKN	2235
	C CA G L DG +C +L+++ L+S+HL E + PF+ +		
Sbjct	2365	TPKCDCAGTQLSDGKNCIASTENFLIPALNSLRSLSLHDPENHS---PPFQTINVERT	2420
Query	2236	VIALAFDYRAGTSPGTPNRIFFSDIHFGNIQGIN---DDGSRRITIVEN-VGSVEGLAY	2290
	V++L +D +RI+F+ +QI+ + G+ T++ + +G+ +G+A+		
Sbjct	2421	VMSLDYD-----SVSDRIFTQNLASVGQGQISYATLSSGJHTPTVIASGIRYTAGDIAF	2473
Query	2291	HRCWDTLYWTSYTTSTITRHTVDQTRPGAFERETVITMSGDDHPRAFVLDCEQNLMFWTN	2350
	D + Y + + + G+ TVI PRA VLD CQ ++W +		
Sbjct	2474	----DWITRRIYYSYDYLNMQINSMAEDGS--NRTVIARV--PKPRAIVLDPQCQGYLYWAD	2525
Query	2351	WNEQHPSIMRALSGANVLTLLIEKDRTPNGLAIDHRAEKLYFSADLTKIERCEYDGSH	2410
	W + H I RA L G + ++ + P+GL +D+ + LY+ DA+L +IER G		
Sbjct	2526	W-DTHAKIERATLGGNFRRVPIVNSSLVUMPSGLTLDYEEIDLWVVDASLQRIERSTLTGVD	2584

Blast Result

Query	2411	RYVILKSEPVHPFGLAVYGEHIFWTDWRRRAVQRANKHVGSNMKLLRVDIPOQQPMGI-IA	2469
R	VI+	+ VH FGL +YG++I+WTD + + RANK+ GS + ++ QP GI	
Sbjct	2585	REVIVNAA-VHAFGLTLYQYIYWTDLYTQRIYRANKYDGSQIAMTTNLSSQPRGINTV	2643
Query	2470	VANDTNSCELSPCRINNGGCQDLCLLTHQGHVNVC--RGGRILQDDLT-CRAVNSSCRA	2526
V	N	C +PC NGGC +C G C C G L++ C N	
Sbjct	2644	VKNQKQQCN-NPCEQFNNGGSHICAPGPN-AECQCPHEGNWYLANNRKHICIVDNGERCG	2701
Query	2527	QDEFECANGECINFSLTCDCGVPHCKDKSDEKPSYCSNSRRCKKTFRQCSNGRCVSNLWCN	2586
F	C+NG CI+	CD C D SDE S C C T C+NGRCV C+	
Sbjct	2702	ASSFTCSNGRCISEEWCNDNDCGDSDEMESVCALHTCSPATAFTCANGRCVQYSYRCD	2761
Query	2587	GADDGCGDSDEIPCNKTACGVG-EFRGRDGTCIGNSSRCNQFVDCED--ASDEMNCSATD	2643
+DCGDSDE	C C EF C + CI CN +C D SDE NC		
Sbjct	2762	YYNDCGDGSDEAGCLFRDNCATTFCMCNRCCIPREFCNGVDFNCHDNNTSDEKNCNPDR	2821
Query	2644	CSSYFRLGVKGVLFQPCERTSLCYAPSVCWDGANDCGDYSERDERCPGVKRPCPLNYFAC	2703
C S +	C ++C + +CDG NDCGD SDE C + F C		
Sbjct	2822	CQSGYT-----KCHNSNICIPRVYLCGDNDGCDGNSDENPTYCTTH-TCSSSEFQC	2871
Query	2704	PSGRCI PMSWTCDKEDDECEHGEDET---HCNKFCSEAQFECQNHRICISKQWLCDGSDDC	2759
SGRCIP	W CD+E DC DE H + C +F+C RCI +W+CDG +DC		
Sbjct	2872	ASGRCI PQHWYCDQETDCFDASDEPASCGHERTCLADEFKCDGGRCIPSEWICDGDND	2931
Query	2760	GDGSDEAAH---CEGKTCGPSSF---PGTHVCVPERWLCDGDKDCADGADESIAAGCL	2813
GD SDE	C+ C S F C P C+P+ W+CDG DC DG DE+ C		
Sbjct	2932	GDMSDDEDKRHQCNQNCSEFLCVNDRPPRCRIPQSVCWDGVDCTDGYDEN--QNCT	2989
Query	2814	YNSTCDRDFMCQNRCQIPKHFVCDHDRDCADGSDESPECEYPTCGPSEFRCANGRCLOSS	2873
TC + EF C	CIPK F CD DC D SDE C Y TC +F C NGRC+S		
Sbjct	2990	-RRTCSNEFTCGYGLCIPKIFRCRDRHNDCGDYSDERG-CLYQTQCNQFTCQNGRCIS-	3046
Query	2874	RQWECDGENDCHDQSDEAPKPNPHCTSQEHKCNASSSQFLCSGRCVAEALLCNGQDDCGDS	2933
++ CD +NDC D SDE C + E C +F C +GRC+ LCN DDC D+			
Sbjct	3047	KTFVCDENDDCDGDSDELMHL--CHTEPEPTC-PPHEFKCDNGRCIEMMKLCHLDDCLDN	3103
Query	2934	SDERGCHINECLSRLKLSGCSQCDCELDLKIGFKCRCPGFRLLKDGRTCADVDECSTT-FPC	2992
SDE+CG INEC	+SGC +C D F C CRPG++ D RTC D+DEC+ F C		
Sbjct	3104	SDEKCGCIGNECHDPSISGCDHNCTDTLTSFYCSRCRPGYKLMSDKRTCVIDECTEMPFVC	3163
Query	2993	SQRQINTHGSKYKCLCVELGYAPRPGGDPHSKCAVTDEEPLIFANRYYLRLKLNLDGSNYTLL	3052
SQ+C N GSY C C GY R D +C+ ++ EP+LIF+NRYYL R +DG Y+L+			
Sbjct	3164	SQKCENVIGSYICKCAPGYL-REPDGKTCRQNSNIEPYLIFNSRNYYLRLNLTIDGYFYSLI	3222
Query	3053	KQGLNNNAVALDFDYREQMIYWTDTVTTQGSMIRRMHLNGNSNVQLHRTGLSNPDGLAVDWV	3112
+GL+N VALDFD	E+ +YW D TQ + I RM LN +N + + L + LAVDNV		
Sbjct	3223	LEGLDNVVALDFDRVEKRLYWIID--TQRQVIERMFLNKTNKETIINHRLPAAESLAVDWV	3280
Query	3113	GGNLYWCDKGRDTIEVSKLNGAYRTVLVSSGLR-----EPRALVVVDVQNGYLYWTDW	3164
LYW D	D + VS LNG +R +L + PR L + Q GYLYW DW		
Sbjct	3281	SRKLYWLDAIRLDGLFVSDLNGHRRMLAQHCVDANNTFCFDNPRLGLAHLPQYGYLYWADW	3340
Query	3165	GDHSLIGRIGMDGSSRSVIVDTKITWPNGNLTQDWTYTER+IYWADEDYIEFASLIGGSNRH	3224
G + IGR+GMDG++S+V+ TK+ WPNG+T+DY + Y+WADA	YIE++ L+G +RH		
Sbjct	3341	GHRAYIGRVRGMDGTNKSVISITKLEWPNGITIDTYTNLDLYWADAHLYGIEYSDLEGHHRR	3400
Query	3225	VVLSQDIPHIFALTLEFEDIVYWTDWETKSINRAHKTGTNKTLLISTLHRPMDLHVFH	3284
V	+PH FA+T+FED +YWTDW T++ + +K G+N+ L+T HRP D+HV+H		
Sbjct	3401	TVYDGalPHPFAITIIFEDTIYWTDWNTTRTVEKGKNGKYDGSNQRTLVNTTHRPFDIHVYH	3460
Query	3285	RQPDVPNPHPCVKVNNGGCSNLCLLSPGG-GHKCACPTNF-YLGSDGRT-CVSNCNTASQFVC	3341
RQP V N PC	NNGGCS+LCL+ PGG G C CP +F L G T C + C+++QF+C		
Sbjct	3461	RQPIVSN-PCCGTNNGGSHLCLIKPGKGKFTCECPDDFRTLQLSGSTYCMPCMSSTQFLC	3519

Query	3342	-KNDKCIPIFWWKCDEDDCGDHSDEPPDCPEFKCRPGQFQCSTGICTNPAPICDGDNDCQ N+KCIPIWWKCD + DC D SDE CP+ CR GQFQCS G CT+P +C+ +C	3400
Sbjct	3520	ANNEKCIPIIWWKCDGQKDCSDGSDELALCPQRFCRLGQFQCSDGNCTSPQTLNAHQNC P	3579
Query	3401	DNSDEAN--CDIHVCLPSQFKCTNTRCIPIGIFRCNGQDNCGDG--EDERDCPEVTCPA N D SDE C+ H C +++C N RCIP ++C+ +C D ED C TC P	3456
Sbjct	3580	DGSDEDRLLCENHHCDSNNEWQCAN-KRCIPIESWQCDTFNDCDNEDEDSHCA SRTCRPG	3638
Query	3457	QFQCSITKRCIPIRVWVCDRNDVCDGSDEP---ANCTQMTCGVDEFRCKDGSRCIPAR W QF+C+ RCIP+W CD DNDC D SDEP + + EF CK + RCIP +W	3512
Sbjct	3639	QFRCA-NGRCIPIQAWKCDVDNDCGDHSDPIEECMSSAHLCDFTEFSCKTNYRCIP-KW	3696
Query	3513	KCDGEDDCGDSDEPKEECDERTCEPY-QFRCKNNRCPGRWQCDYDNDCGDSDEE SCT + + C+E RTC P FRCKN C+P RWQCD NDGDSDEE+C	3571
Sbjct	3697	-AVCNGVDDCRDMSDEQGCEERTCPVGDRCKNHHICPLLRQCDQNDGDSDEENCA	3755
Query	3572	PRPCSESEFSCANGRCIAAGRWKCDGDHDCADGSDEKDCTPR-CDMDQFQCKSGHC IPLRW PR C+ESEF C N +CI RW CD +DC D SDE+DC R C + FOC SGHC+	3630
Sbjct	3756	PRECTESEFRCVNNQQCIPSRWICDHYNDCGDSDERDCEMRTCHPEYFQCTSGH CVHSEL	3815
Query	3631	RCDADADCMGDSDEEACGTGV---RTCPLEFQCNNTLCKPLAWKCDGEDDCG DSDENP +CD ADC+D SDE C T C F+C N +C P WKCDG+DDCGD SDE	3687
Sbjct	3816	KCDGSADCCLASDEADCPTRFPDGAYQATMFECKNHCIPPLYWKCDGDDDCG DSDEEL	3875
Query	3688	EECARFVCPNPFRCKNDRVCLWIGRQCDGTDNCGDTDEEDCEPPTAHTTH CKDKKEF C C FRC N+R C++ C+G D+CGDTDE + C + E+ Sbjct	3747
Sbjct	3876	HLCLDVPCCNSPNRFRCDNNR-CLYSHEVCNVDDCGDTDEEEHCRKPTPK CCT-YEY	3933
Query	3748	LCRNQRCLSSSLRCNMFFDCGDSDEEDCSIDPKLTSCATNASICGDEAR CVRTEKAAY-C N C+ C+ DDCGD SDE C+ K +CA N IC E C + + + Sbjct	3806
Sbjct	3934	KCGNGHICPHDNVCDADDGDSWEGLCN-KGKERTCA EN--IC--EQNCTQLNEGGFI	3988
Query	3807	CACRSGFH-T-VPGQPGCDINECLRGFTSQLC NNTKGGHLCSARNFM---KTHNTCK C+C +GF T V + C DINEC +FGTC Q C NTKG + C CA F + C Sbjct	3861
Sbjct	3989	CSCTAGFETNVDRTSCLINECEQPGT CQHCRNTKGSYECVCADGFTSMSDRPGKRCA	4048
Query	3862	AEGSEQYQVLYIADDNEIRSL-FPGPHPS AEGS +L + D+ IR S Y Q + ++ V D + VI+T Sbjct	3920
Sbjct	4049	AEGSS-PLLLPDVNIRKYNLSSRF SERVSYLQDEEYIQAVDYWDPKD IGLSVVYTTVRG	4107
Query	3921	TGTISYRSLLPAA PPTTSNRRHQPI IDRGRVTHLNISGLKMP PRGIAIDWVAG NQYWTDSGRD G+ + ++ A P + + L + + P GIA+DWV ++Y+D Sbjct	3980
Sbjct	4108	EGS-RFGAIKRAYIPNF ESGRNNLVQE--V DLKLKYVMQ PDGIAVDWVGR HIYWSDV VKNK	4164
Query	3981	VIEVAQMKG ENRKT LISGM IDEPAH IVV DPLRG TMW WSDW GNH PKI ETAA MDGT LRET LV IEVA++ G RK LIS +D+P AI V+P G M+ W+D NG PKI E+A M+G R LV RIEVAKLD G RYRK WL IST L DQ P AA IA V N PKL GLM FW TD WG KE PK IES A WM NG ED RN IL V	4040
Sbjct	4165	RIEVAKLD G RYRK WL IST L DQ P AA IA V N PKL GLM FW TD WG KE PK IES A WM NG ED RN IL V	4224
Query	4041	QDNIQW PTGLAVD Y-HNERLY WADAKL S SV IGS SIR LN G TDP IV A ADS SK R GL SH P FS ID V F E +++ W PTGL + +D Y + +N+R+Y+D K V I + +GTD V A + +P+S+D+F E F EDL GW PT GLS I D Y LN N D R I Y Q D F E V I E T I K Y G T D R V I A -- KEAM NP I S L D I F E	4099
Sbjct	4225	FEDLGW PT GLS I D Y LN N D R I Y Q D F E V I E T I K Y G T D R V I A -- KEAM NP I S L D I F E	4281
Query	4100	DYIYG TYIN NRRV FI KHK FGH SPL VNL T G L S H AS DV V LY HQ HK -Q P EV T N P C DR KK CE W D + Y ++ V + K + F G + V + H Q + V N C ++ C L Y W I S K E G V W Q K N P L C -K Q I C H S H	4158
Sbjct	4282	TD Q R Y W I S K E G V W Q K N P L C -K Q I C H S H	4340
Query	4159	LCLLSP GP V CT CP NG K L D N G T C V P V P S P T P P D A P R P G T C N L Q C P N G G S C F L N A R R Q P L C L C L R P G G Y S C A P Q G S S F I E G S T T C D A A I E L P I N L P P -- P C R C M H G G N C Y F D E T D L P P	4218
Sbjct	4341	LCLLSP GP V CT CP NG K L D N G T C V P V P S P T P P D A P R P G T C N L Q C P N G G S C F L N A R R Q P L C L C L R P G G Y S C A P Q G S S F I E G S T T C D A A I E L P I N L P P -- P C R C M H G G N C Y F D E T D L P P	4397
Query	4219	KCRCQ P R Y T G K C E L 4233	
Sbjct	4398	KCKCPS G Y T G K Y C E M 4412	



Score = 595 bits (1535), Expect = 4e-167
 Identities = 372/1068 (34%), Positives = 536/1068 (50%), Gaps = 88/1068 (8%)

Query 840	VTCLANPSYVPPPQQCOPGEFACANSRCIQUERWKCDGNDNCLDNNSDEAPALCHQHTCPNSDR	899
V CLA S	+C F C + CI W+CDG DC D++DE C TC	
Sbjct 17	VACLAPAS---GQECDSAHFRCGSGHCIPADWRCDGTKDCSDADEIG--CAVVTCCQGY	71
Query 900	FKCENN-RCIPNRWLCDGDNDCGNSEDESNAUTCSARTCPNPQFSCASGRICIPISWTCLDLDFKC++ +CIPN W+CD D DC + DE CS TC +Q +C+G+CIP + CD	958
Sbjct 72	FKCQSEGQCIPNSWVCDQDCDGSDERQ-DCSQTCSHSQITCSNGQCIPSEYRCDHV	130
Query 959	DDCGDRSDESASCAYPTCFPLTQFTCNNGRCININWRCDDNDCGDNSDEAGCSHSCSST DC D +DE+ C YPTC Q TC+NG C N + +CD DC D+SDE C+ C	1018
Sbjct 131	RDCPDGADEN-DCQYPTC--EQLTCDNGACYNTSQKCDWKVDCRDSDEINCTEBICLHN	186
Query 1019	QFKCNSGRCIPEHWTCDGDNDCGDYSDETHANCTNQATRPPGGCHTDEFQCRLDGLCIPL +F C +G CIP + CD DNDC D SDE N C +F C G CI	1078
Sbjct 187	EFPSGNCECIPRAYVCDHNDQDCDGSDEHACNYPT-----CGGYQFTCP-SGRCIYQ	237
Query 1079	RWRCDGDTDCMDSSEKSCEG---VTHVCDPSVKFGCKDSARCISKAWVCDGDNDCEDNS W CDG+ DC D+ DE CE H C P ++ C +S RCIS VCDG	1135
Sbjct 238	NWVCDGEDDCKDNGDEDGCESGPVDHKVCSPR-EWSCPESGRCISIYKVCDBG-----	288
Query 1136	DEENCESLACRPPSHPCANNTSVCLPPDKLCGDGNDCDGDSDEGELCDQCSLNNGCASHN L C P NNTS + CS N C +	1195
Sbjct 289	-----ILDC--PGREDENNNTST-----GKYCSMTLCSALN--CQYQ	320
Query 1196	CSVAPGEIVCSCPGLMELG-PDNHTCQIQSYCAKHLKCSQKCDQNKFVKSVCSCYEGWVL C P G C CP G + D+ TC C C QKC+ C C EG++L	1254
Sbjct 321	CHETPYGG-ACFPCCPGYIIHNDNSRTVCVEFDDCQIWGICDQKCESRPGRHLCHCEEGYIL	379
Query 1255	EPDGESCRSLDPF-KPFIIFSNRHEIRRIDLHKGDYSLVPLGRNNTIALD--FHLQSAL E G+ C++ D F + IIFSN ++ D+H + +LV +A+ FH +	1311
Sbjct 380	E-RGQYCKANDSFGEASIIFSNGRDLIICDIHGRSFRILVESQNRGVAVGVAFHYHLQRV	438
Query 1312	YWTDVVEDKIYRGKLLDNGALTSFEVVIQYGLATPGLAVDVIAGNIYWVESNLQDQIEVA +WTD V++K++ + NG + + V+ + TPE LAVDW+ IY VE+ + +I++	1371
Sbjct 439	FWTDTQNKVFSVDI--NG--LNIQEVLNVSVETPENLAVDWVNPKIYLVETKVNRIIDMV	494
Query 1372	KLDGTLRTTLLAGDIEHPRAIALDPRDGILFWTDWD--ASLPRIAASMSGAGRRTVHRE LDG+ R TL+ ++ HPR IA+DP G LF++DW+ + P+E A M G+ R+ + +	1429
Sbjct 495	NLDGSYVRTLITENLGHPRGIAVDPVTGYLFFSDWESELSCGEPKLERAFMDGSNRKDLVKT	554
Query 1430	TGSGGWPNGLTVDYLEKIRWLHIDARSDAIYSARDGSGHMEVLRGHEFLSHPFAVTLYGG GWP G+T+D + KR+ W+D+R D I + YDG V+ G + HFP V+L+ G	1489
Sbjct 555	--KLGPWAGVTLDMISKRVYVWDSRFDYIETVTDG1QKRKTVVHGGSЛИPHPFGVSLFEG	612
Query 1490	EVYWTDWRTNTLAKANKWGHNVTVVQRTNTQPDFLQVYHPSRQPMAPNPCEANGQQGPC +V++TDW + KANK-T N V + + +P+ + VYH RQP A NPC+ N G C	1549
Sbjct 613	QVFPTDWTKMAVLKANKFETTNPQVYYQASLRPYGVTVYHSLRQPYATNPCKDN--NGC	670
Query 1550	SHLCLINYNRT----VSCACPHMLKLHKDNTTCYEFKKFLLYARQMEIRGVLDAPYNN +C+++ C C +L D C + FL+++ Q+ IRG+	1604
Sbjct 671	EQVCVLSHRTDNDGLGFRCKTGFQQLDTDERHClAQVNFLIFSSQVAIRGIPFTLSTQE	730
Query 1605	YIISFTWPDIIDNVTVLDYDAREQRVYWSDVRQAICRAFINGTGVETVVSADLPAHGLA ++ + +D+DA++ ++SD+ I + I+GTG E + + + N LA	1664

Blast Result

Sbjct	731	DVMVPVSGNPSFFVGIDFDAQDSTIFFSDMSKHMIFKQKIDGTGREIILAANRVENVESLA	790
Query	1665	VDWWSRNLFWTSYDTNKQINVARLDGSFKNAVVGQLEQPHGLVHPLRGKLYWTD--G DW+S+NL+WT D++ K I+V RL + VVQ L P +VWHP G L++TD	1721
Sbjct	791	FDWISKNLWWT--DSHYKSISVVMRLADKTRRTVVQYLNPPRSVVVHPFAGYLFFTDWFPRP	848
Query	1722	DNISMANMDGSNRTLLFGSQKG-PVGLAIDFPESKLYWISSGNHTINRCNLDGSGLEVID I A DGS+ + + G P GLAID+ S+LYW+ + I DG +	1780
Sbjct	849	AKIMRAWSDGSHLLPVINTTLGWFNGLADWAASRLYWVDAYFDKIEHSTFDGLDRRLG	908
Query	1781	AMRSQLGKATALAIMGDKLWADQVSEKMGTCSDKADGSSGVVLRNSTTLMVHHMKVYDESI + Q+ LAI G L++ D + KADG V+R+ ++H+K YD + I	1840
Sbjct	909	HI-EQMPHTPGLAIFGEHLFFTDWRLGAIIVRVKADGGMETVIRSGIAYILHLKSYDVNI	967
Query	1841	QLDHKGTNPCSVNNGDCSQLCLPTSETTRSCMCTAGYSLRSQQACBG Q N + NGDCS C P R C C G L S CEG	1888
Sbjct	968	QTGSNACNQPTHPNGDCSHFCFPVPNFQRVCVGCPTYGMRLASNHLTECG	1015



Score = 428 bits (1100), Expect = 1e-116
 Identities = 261/716 (36%), Positives = 367/716 (51%), Gaps = 56/716 (7%)

Query	2640	SATDC-SSYFRLGVKGVLFPQPCERTSLCYAPSVCDFGANDCGDYSDERDCPGVKRPICPL	2698
Sbjct	24	S +C S++FR G + C W CDG DC D +DE C V C SGQECDSAHRFCG-----SGHCIPADWRCDGTKDCSDADEIGCAVVT---CQQ	69
Query	2699	NYFACPS-GRCIPMSWTCDFKEDDCEHGEDETH-CNKF-CSEAQFECQHNRCISKQWLCDG YF S C G+CP SW SD++ DC+ G DE C++ CS Q C N +CI ++ CD	2755
Sbjct	70	GYDKCQSEQCP1QNSWVCDQDQDCDGSDEHQDCSQSQTCSHHQITCSNGQCIPSEYRCDH	129
Query	2756	SDDCGDGSDEAAHCEGKTCGPSSFCGPHTHVCVPERWLCDGDKDCADGADESIAAGCLYN DC DG+DE C+ TC +C + + + CL+N	2815
Sbjct	130	VRDCPDGADEN-DCQYPTC-EQLTCDNGACYNTSQKCDWVCDRCDSSDEINCTEICLHN	186
Query	2816	STCDREFFMCQNRRQCIPKHFVCDHDRCADGSDESPECEYPTCPSEFRCANGRCLSSRQ EF C N +CIP+ +VCDHD DC DGSDE C YPTCG +F C +GRC+ +	2875
Sbjct	187	-----EFSCGNNGECIPRAYVCDHDNDCQDGSDDEHA-CNYPTCGGYQFTCPSPGRCIY-QN	238
Query	2876	WECDGENDCHDQSDE--APKNPHCTSQEHNKCNASSSQFLCSSGRCAVAEALLCNGQDDCGDS W CDGE+DC D DE PH HKC+ SGRC++ +C+G DC	2933
Sbjct	239	WVCDGEDDDCKDNGDEDGCGESGPB--DVHKCSPREWSCPSEGRCSICISIYKVDGILDCPGR	295
Query	2934	SDERGCHINECLSRKLSSG--CSQDCELDKIGFKCRCRPGFLRK-DDGRTCADVDECSTT DE + S L C C + G C C PG+ +D RTC + D+C	2989
Sbjct	296	EDENNNTSTGKYCSMTLCSALNCQYQCHETPYGGACFCPPGYIINHNDNSRTCVFEDDCQIW	355
Query	2990	FPCSORCINTHGSYKCLCCLVEGYAPRGGDPHSCKAVTD-EEPFLIFANRYYLRLKNLDGSN C Q+C + G + C C EGY G CKA E +IF+N L ++ G +	3048
Sbjct	356	GICDQKCESRPGRLCHCEEYGILERQ--YCKANDSFGEASIIFSNGRDLLIGDIHGRS	413
Query	3049	YTLLKQGLNNAVALD-FDYREQMIYWTDTVTTQGSMIRRMHLNGSNVQLHRTGLSNPDG + L+ N VA+ E Y Q ++WTD T + + +NG N+Q + + P+	3106
Sbjct	414	FRILVESQNRGVAVGAVPHYHLQRVFTD-TVQNKVFSVDINGLNQEVLMVSVETPEN	471
Query	3107	LAWDWVGGNLYCWDKGDRDITIEVSKLNGAARYTTLVWVSSGLREPRALVVDVQNGLYWTDWGD LAWDWV +Y + + I++ L+G+Y RT L++ L PR + VD GYL++DW	3166
Sbjct	472	LAWDWVNKNIYLVETKVNIDMVNLGDSYRVTLITENLGHVPRGIAVDPVTGVLFFSDWES	531
Query	3167	HS--LIGRIGMDGSSRSVIVDTKITWPNGLTLDYVTERIYWADAREDYIEFASLDGSNR	3223

Blast Result

Sbjct	532	S + R MDGS+R +V TK+ WP G+TLD +++R+YW D+R DYIE + DG R LSGEPKLERAFMDGSNRKDLVKTKLGWPAGVTLDMISKRVYVWDSRFDYIETVTDYGIQR	591
Query	3224	HVV1--SQDIPHIFALTLFEDYVYWTWETKSINRAHKTGTNKTLLISTLHPRPMDLHVF V+ IIPH F ++LF E V++TDW ++ A+A K T TN + RP + V+	3281
Sbjct	592	KTVVHGGLSLIPHPPFGVSLFEGQVFFDTWKMAVLKANKFTETNPQVYYQASLRPYGVTVY	651
Query	3282	HALRQPDPVNHPCKVNNNGGSNLCLLS----PGGGHKACPTNFYLGSDFGRTCVS H+LRQP N PCK NNGGC +C+LS G G +C C F L +D R C++	3332
Sbjct	652	HSLRQPYATN-PCKDNNGGCEQVCVLSHRTDNDGLGFRCKCTFGFQLDTERHCIA	706



Score = 376 bits (966), Expect = 4e-101
 Identities = 267/841 (31%), Positives = 407/841 (48%), Gaps = 58/841 (6%)

Query	24	PKTCSPKQFACRDQITCISKGWRCDGERDCPDGSDEAPEICPQSKAQRCQNEHNCLGTE PKTC F C D CI + W CD + DC D SDE CP ++ RC + CLG	83
Sbjct	1268	PKTCPSYFHC-DNGNCIHIRAWLCDRNDGDMDSDEKD---CP-TQPFRCPSWQQLGHN	1323
Query	84	LCVPMSRLCNGVQDCMDGSDEGPCHCRELQNCNSRLGCOHHCVPTLDGPTCYCNSSFOLQA +CV +S +C+G DC +G+DE P C + GC H CV G C C F L	143
Sbjct	1324	ICVNLSVVCDFIDFCPNGTDESPLCNGNSCSDFNNGGCTHECVQEPFGAKCLCPLGFLAN	1383
Query	144	DGKTCDFDECVSYGTCSQLCTNTDGSFICGCVEGYLLQPDNRSCAKNEPVDRPPVLLI D KTC+D DEC + G+CSQ C N GSF C C GY++ D R+CK +LL+	203
Sbjct	1384	DSKTCEDIDECDILGSGSCQHCVNMRGSFRCSCTGYMLESDGRTCKV---TASESLLLV	1440
Query	204	ANSQNILA-TYLSGACQVSTITPTSTQTTCATMDFSYANETCCTVWVHVGDAAQTQLKCARMP A+ I+A + S + A+DF + W A Q + A	262
Sbjct	1441	ASQNKKIADSVTSQVHNIIYSLVENGSIYIVAVDFDSISGRIFW---SDATQGKTWSAFQ	1496
Query	263	GLKGFBVDEHTINISLSSLHHVEQMAIDWLGNFYFVDDIDDRIFVCNRNGDTCVTLLDLEL G + + S+ E +AIDW+ N Y+ D + I V +G L+ L	322
Sbjct	1497	G-----TDRRVVFDSIIILTETIAIDWVGGRNLYWTDYALETIEVSKIDGSHRTVLISKNL	1551
Query	323	YNPKGIALDPAMGK--VFFTIDYQKIPKVERCDMDGQNRKTLVDSKIVFPHGITLDLVSR NP+G+ALDP M + F++D+G P++ER MDG RT +V KI +P G+T+D +RL	380
Sbjct	1552	TNPRLGALDPRMNEHLLFWSDWGHHPERRASMDGSMRTVIVQDKIFWPCGLTIDYPNRL	1611
Query	381	VYWAALYLDVYVVDYEG-KGRQTI IQGILIEHLHYGLTVFENLYATNSDNANAQQKTSV +Y D+YLDY++ DY G RQ I +I H Y LT+FE+ +Y T D A + V	439
Sbjct	1612	LYFMDSYLDYMDFCYDNGHHRQVIASDLIIRHPYALTLEFDVSYWT--DRATRR---V	1665
Query	440	IRVNRFNSTEYQVVT-RVDKGALHIYHQRQPRPVRSHACENDQYKGPGGCSDICLLAN- +R N++ VV + + H +QP + C + CS +CLL++	497
Sbjct	1666	MRANKWHGGNQSVMYNIQWPLGIVAVHPSKQPN-SVNPCAFSR-----CSHLCLLSSQ	1718
Query	498	SHKARTCRCSRGFSLGSKGSKCKPEHEFLVYKGKRPGLIIRGMGMAKV-PDEHMIPIE +C C SG+SL D +C + + R II G+ + V + M+PI	556
Sbjct	1719	GPHFYSCVCPGWSLSPDLLNCLRDDQPFPLITV--RQHIIIFGISLNPEVKSNDAMVPIA	1775
Query	557	NLMNPNALDFHAETGFIYADFTTSYLIQGKQKIDTERETILKDGHINNE-GVAVDWMGDN + N + +F +YI + + I R K DGT R + +A+DW+ N	615
Sbjct	1776	GIQNLGDLDFEADAEQYIYWWENPGE-IHRVKTDTGNTVFAFISMVGPSMNLALDWISRN	1834
Query	616	LYWTDDGPKKTISVARLEKAQTRKTLIEGKMT----HPRAIVVDPLNGWMYWTDWEE LY T+ ++I V L + RKTLL T P I VDP G +YW+D D	670
Sbjct	1835	LYSTNP-RTQSIEVLTLLHGDIDYRKTLLIANDGTALGVGFPIGITVDPARGKLYWDQGTD	1893

blast result

Query	671	PKDSRRGRLERAWMDG-SHRDIFVTSKTVLWPNGLSSLIDIPAGRPLYWVDAFYDRIETILLN	729
		++ A MDG S +F + L ++LDI +LYW IE ++	
Sbjct	1894	--SGVPAKIASANMDGTSVKTLFTGNLLEHL--ECVTLDIEEQKLYWAVTGRGVIERGNVD	1949
Query	730	GTDRKIVYEGPELNHAFLCHHGNYLFWTEYRSGSVYRLERGVGGAPPTVTLRSERPPI	789
		GTDR I+ +L+H +G+ H ++L++T+ + R+++ G +LR P +	
Sbjct	1950	GTDRMILVH--QLSHPGWIGIAVHDSPFLYTTDBQEYEVIERVDKATGA---NKIVLRDNVPNL	2004
Query	790	FEIRMYDAQQQQVGNTNKRVNNGCSSLCLATPGSR-QCACAEQVLDADGVTCANPSY	848
		++Y + +N C N C +CL PG CACA L+ D +C S+	
Sbjct	2005	RGLQVYHRRNAESSNGCSNNMNACQQICLPVPGFLFSCACATGFKLNPDRNRSCSPYNSF	2064
Query	849	V 849	
		+	
Sbjct	2065	I 2065	



Score = 320 bits (819), Expect = 4e-84

Identities = 219/745 (29%), Positives = 324/745 (43%), Gaps = 93/745 (12%)

Query	3453	CAPNQFQCSITKRCIPRWWVCDRNDVCGSDEPANCTQMTCGVDEPRCKDSGRCPARW	3512
		C F+C + CIP W CD DC D +DE C +TC F+C+ G+CIP W	
Sbjct	28	CDSAHRFCG-SGHCPIDPWRCDGTCDCSDDADE-IGCAVWTCCQGYFKCQSEQCIIPNSW	85
Query	3513	KCDGEDDCGDGSDEPKECERTDCEPYQFRCKNNRCPVGRWQCDYDNDCGDNSDEESCTP	3572
		+D D + ++C + TC +Q C N +C+P ++CD+ DC D +DE C	
Sbjct	86	-VCDQDQDCDDGSDERQDCSQTCSHSQHTCNSGQCIPSEYRCDHVRDPGADENDCQY	144
Query	3573	RPCSESEFSCANGRCIAGRWKCDGDHDCADGSDEKDCTPRCDMDPQCKSGHCIPLRWRC	3632
		C + +C NG C KCD DC D SDE +CT C ++F C +G CIP + C	
Sbjct	145	PTCBB--LTCDCNGACYNTSQKCDWKVDCRDSSDEINCTEICLHNEFSCGNGECPRAYVC	202
Query	3633	DADADCMDGSDEEACGTGVRTCPLEDFQCNNTLCKPLAWKCDGDEDDCGDNSDENPEECAR	3692
		D D DC DGSDE AC TC +F C + C W CDGEC DC DN DE+ E	
Sbjct	203	DHDNDQDQDCGSDEHACN--YPTCGGYQFTCPGSGRCIYQNWWCDGEDDCDKNGDEDGESG-	259
Query	3693	FVCPPNRPFRKNCNRVCLWIGRQCDGTDNCGDTDEEDCEPPATAHTTHCKDKKEFLC-RN	3751
		H H +E+ C +-----PHDVHKCSPREWCPE	
Sbjct	260	-----	276
Query	3752	QRCLSSSLRCNMFPDCGDSDEEDCSIDPKLTSCATNASICGDEARCVRTEAAACCRS	3811
		RC+S C+ DC DE + S + +A C + +C T C C	
Sbjct	277	GRCISIYKVCGDILDCPGREDENNTSTGKYCSMTLCSALNC--QYQCHETPYGGACFCPP	334
Query	3812	GFHTVPGQPG-CQDINECLRFGTCSQLCNNTKGHLCSCARNF-MKTHNTCKAEGSEYQV	3869
		G+ C + ++C + G C Q C + G HLC C + ++ CKA S +	
Sbjct	335	GYIINHNSRTCVFEDDCQIWGICDQKCESRPGRHLCHCEEGYIILERGQYCKANDSFGEA	394
Query	3870	LHYIADDNEIRSLFPGHPHS-AYEQAQFGDESVRIDAMDVHVKGAGRVYWTNNHTGTISYRS	3928
		I + R L G H ++ + + H RV+WT+	
Sbjct	395	SIIFTSNG--RDLLIGDIHGRSPRILVESQNRGVAVGVAFYHLQRVFWTD-----	442
Query	3929	LPPAAPFTTSNRHRRQIDRGVT---HLNISGLKMPRGIAIDWVAGNVYWTDSGRDVIEVA	3985
		T N+ G+ LN+S ++ P +A+DWV +Y ++ + I++	
Sbjct	443	-----TVQNKVFSVDINGLNQIEVLNVS-VETPENLAVDWWNNK1YLVETKVNRIDMV	494
Query	3986	QMKGENRKTLLISGMIDEPAHVVDPLRGTMWSD--GNHPKIETAMDGLTRLTLVQD	4042
		+ G R TL+ + P I VDP G +++SDW PK+E A MDG+ R+ LV+	
Sbjct	495	NLDGSTYRTLITENLGHPRGIAVDPTVGYLFPSDWESELSGEPKLERAFMDGSNRKDLVKT	554

blast result

Query 4043	NIQWPTGLAVDHYNERLYWADAKLSVIGISIRLNGTDDPIVAADSKRGLSHPFSIDVFEDYI + WP G+ +D ++R+YW D++ I ++ +G + HPF + +FE +	4102
Sbjct 555	KLGWPAGVTLDIMISKRVVWVDSRFDYIETVTYDGIQRKTVVHGGSLIPHFGVSLFEGQV	614
Query 4103	YGVTYINNRVFKIHKGH-SPLVNLTGGLSHASDVVLYHQHKQPEVTNP--DRKKCEWL + + V K +KF +P V L V+YH +QP TNPC + CE +	4159
Sbjct 615	FPTDWTKMAVLKANKFTETNPQVYYQASL-RPYGVTVHSLRQPYATNPCKDNNGCEQV	673
Query 4160	CLLSPS-----GPVCTCPNGKRLD 4178	
C+LS	G C C G +LD	
Sbjct 674	CVLSHRTDNDGLGFRCKCTFGFQLD 698	



Score = 263 bits (671), Expect = 6e-67
 Identities = 166/497 (33%), Positives = 253/497 (50%), Gaps = 40/497 (8%)

Query 25	KTCSPKOFACRDQITCISKGWRCDGERDCPDGSDEAPEICPQSKAQRCQPNENHNCGLTEL +TC QF C++ CISK C+CD +DC DGSDE +C + C P+E C	84
Sbjct 3030	OTCQCNQFTCQNG-RCISKTFVCDENDCCDGDSDELMHLC-HTPEPTCPHFKC-DNGR	3086
Query 85	CVPMSRLCNGVQDCMDGSDE-GPHCRELQGNCSRLGCQHHCVPTELDGPTCYCNSSFQLQA C+ M +LCN + DC+D SDE G E + S GC H+C TL C C ++L +	143
Sbjct 3087	CIEMMKLCNHLDCLDNSDEKGCGINECH-DPSISGCDHNTDTLTSFYCSCRPGYKLM	3145
Query 144	DGKTCKDFDECSVYG-TCSQLCTNTDGSFICGCVEGYLLQPDNRSCAKNEPVDRPPVLL D +TC D DEC+ CSQ C N GS+IC C GYL +PD ++C+ +N ++ P L+	202
Sbjct 3146	DKRTCVDIDECTEMPFVCSQKCENVGISYICKCAPGVLREPDGKTCR-ONSIE--PYLI	3202
Query 203	IANSQNILATYLSGAQVSTITPTSTRQTAMDFSYANETVCWVHVGDSAQQTQLKCARMP +N + + G S I A+DF + + W+ TQ +	262
Sbjct 3203	FSNRYYLRLNTIDGYFYSLILEGLDNVV-ALDFDRVEKRLYWI-----DTQRQVIERM	3254
Query 263	GLKGFDVDEHTINISLSSHVQEAMAIDWLTLGNFYFVDDIDDRIFVCNRNG-----DTCV L E IN L E+A+DW++ Y++D D +FV + NG CV	315
Sbjct 3255	FLNKTNKETIINHRLPA---AESLAVDWWRSRKLYWLDARLGLFVSDLNGGHRRMLAQHCV	3312
Query 316	TLLDLELY-NPKGIALDPAMGKVFFTDYQGQIPKVERCDMDQNRKTLVDSKIVFPHGITL + + NP+G+AL P G +++ D+G + R MDG N++ ++ +K+ +P+GIT+	374
Sbjct 3313	DANNTFCFDNPRGLALHPQYGYLYWADWGHRAYIGRVGMGDTKNSVIISTKLEWPNGITI	3372
Query 375	DLVSRLVWADAYLDYIEVVVDYEGKGKRQTIIOQGILIEHLYGLTVFENLYATNSDNANAQ D + L+YWADA+L YIE D EG R T+ G L H + +T+FE+ +Y T+ +	434
Sbjct 3373	DYTNDLLYWADAHGLGYIEYSDLEGHHRHTVYDGAL-PHPFAITIFEDTIYWTDWNT----	3427
Query 435	OKTSVIRVNRFNSTEYQ-VVTRVDKGALHIYHQRRQPRVRSHACENDQYKGPGGCSDIC +V + N+++ + Q +V + +H+YH RQP V + N+ GGCS +C	493
Sbjct 3428	--RTVEKGKNUYDGSNRQTLVNTTHRPFIDHVYHYPYRQPIVSNPCGTNN----GGCSHLIC	3480
Query 494	LLANSHKARTCRCRSGF 510	
Sbjct 3481	L+ K TC C F LIKPGGGKFTCECPDDF 3497	



blast result

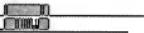
Score = 220 bits (561), Expect = 3e-54
 Identities = 113/286 (39%), Positives = 148/286 (51%), Gaps = 12/286 (4%)

Query	3413	CLPSQFKCTNTNRCIPGIFRCNGQDNCGDGERDCPEVTCAVNQPCQCSITKRCIPRVWV	3472
	C	+ F+C + CIP +RC+G +C D DE C VTC F+C +CIP WV	
Sbjct	28	CDSAHRFC-GSGHCIPADWRCDGTKDCCSDDAEIGCAVVTQQGYFKCQSEGQCIPNSWV	86
Query	3473	CDRNDCDCVGDGSDEPANCTQMTCGVDFEPRCKDGSGRCPARWKCDGEDDCGDSDEPKEECD	3532
	CD+D DC DGSDE +C+Q TC + C +G+CIP+ ++ + + +C		
Sbjct	87	CDQDQDCDDGSDERQDCSQTCSHSQITC-SNGQCIPSEYR--CDHVRDCPDGADENDCQ	143
Query	3533	ERTCEPYQFRCKNNRVCVPGRWQCDYDNDGDNSEESCTPRPCSESEFSCANGRCIAGRWTCE Q C N C +CD+ DC D+SDE +CT C +EFSC NG CI +	3592
Sbjct	144	YPTCE--QLTCDNGACNTSQKCDWKVCDRDSSEINCT-EICLHNEFSCGNGECPRAY	200
Query	3593	KCDGDHDCAGSDEKDCT-PRCDMDQFQCKSGHCHIPLRWRCDADACMDGSDEEACGTG-CD D+DC DGSD E C P C QF SG CI W CD + DC D DE+C G	3650
Sbjct	201	VCDHDNDQDGSDHEACNYPTCGGYQPTCPSPGRCIYQNWVCDGEDDCKDNGDDEGCESGP	260
Query	3651	--VRTCPLDEFQC-NNTLCKPLAWKCDGEDDCGDSDENPEECARF 3693	
	V C E+ C + C + CDG DC DEN ++		
Sbjct	261	HDVKHKS PREWSCPESGRCISIYKVCDGILDCPGREDENNTSTGKY	306



Score = 209 bits (532), Expect = 8e-51
 Identities = 123/350 (35%), Positives = 166/350 (47%), Gaps = 41/350 (11%)

Query	3373	KCRPGQFQCSCTGICTNPAFICDGDNDQCDNSDEANCDIHVCLPSQFKCTNTNRCIPGIFR	3432
	+C F+C +G C + CGD DC D+DE C + C FKC + +CIP +		
Sbjct	27	ECDSAHFRCGSGHCIPADWRCDGTKDCCSDDAEIGCAVVTQQGYFKCQSEGQCIPNSWV	86
Query	3433	CNGQDNCGDGEADER-DCPEVTCAVNQPCQCSITKRCIPRVWVCDRNDCDCVGDGSDEPANCTQ	3491
	C+ +C DG DER DC +TC+ +Q CS +CIP + CD DC DG+DE +C		
Sbjct	87	CDQDQDCDDGSDERQDCSQTCSHSQITC-NNGQCIPSEYRCDHVRDCPDGAE-NDCQY	144
Query	3492	MTCGVDFEPRCKDGSRCIPARWKCDGEDDCGDSDEPKEECDERTCEPY---QFRCKNNRTC ++ C D+G C KCD + DC ++ DE C +F C N	3547
Sbjct	145	PTC--EQLTC-DNGACNTSQKCDWKVDC-----RDSSDEINCTEICLHNEFSCGNGE	194
Query	3548	CVPGRWQCDYDNDGDNSEESCTPRPCSESEFSCANGRCIAGRWKCDGDHDCAGSDEK	3607
	C+P + CD+DNDC D P+C C +F+C +GRCI W CDG+ DC D DE		
Sbjct	195	CIPRAYVCDHDNDQDGSDHEACNYPTCGGYQPTCPSPGRCIYQNWVCDGEDDCKDNGDED	254
Query	3608	DC-----TPRCMDMDQFQC-KSGHCIPLWRWCDADACMDGSDEEACGTGVRTCPLDEFQ	3660
	C + +C + +G CI + CD DC DE TG		
Sbjct	255	GCESGPHDVHKKS PREWSCPESGRCISIYKVCDGILDCPGREDENNTSTGK-----Y	306
Query	3661	CNNTLCKPLAWKCDGEDDCGDSDENPEECARFVCPNRPFRCKNDRVCL	3710
	C+ TLC L +C E P A F CPP + R C+		
Sbjct	307	CSMTLCSAL-----NCQYQCHETPYGGACF-CPPGYIINHNDNSRTCV	347



Score = 174 bits (440), Expect = 4e-40
 Identities = 107/302 (35%), Positives = 135/302 (44%), Gaps = 55/302 (18%)

Query	3331	VSNCTASQFVCKND-KCIPFWVKCDTEDDCGDHSDEPPDCPEFKCRPGQFQCSTGICTNP V C F C++ +CIP W CD + DC D SDE DC + C Q CS G C	3389
Sbjct	64	VVTCCQGYFKCQSEGQCIPNSWVCDQDQCDGSDERQDCSOSTCSSSHQITCSNGQCIPS	123
Query	3390	AFICDGDNDCQDNSDEANCDIHVCLPSQPKFTNTNRCPGIFRCNGQDNCGDGEDERDCP + CD DC D +DE +C C Q C N C +C+ + +C D DE +C	3449
Sbjct	124	EYRCDHVRDCPDGAENDCQYPTC--EQLTCDN-GACYNTSQKCDWKVDCRDSSDEINCT	180
Query	3450	EVTCAPNQFQCSITKRCIPIRVWVCDRNDVCGDSDEPANCTQMTCGVDEFRCKDGSRCIP E+ C N+F C CIPR +VCD DNDC DGSDE A C TCG +F C SGRCI	3509
Sbjct	181	EI-CLHNNEFSCG-NGECLIPRAYVCDHDNDCQDGSDEHA-CNYPTCGGYQFTC-PSGRCI-	235
Query	3510	ARWKCDGEDDCGDSDEPKEECDERTCEPYQFRCKNNRCPGRWQCDYDNDCGDANSDEES YQ W CD ++DC DN DE+-----YQ-----NWVCDGEDDCDKDNGDEDG	3569
Sbjct	236	-----YQ-----NWVCDGEDDCDKDNGDEDG	255
Query	3570	CTPRP-----CSESEFSC-ANGRCIAGRWCDCGDHDCADGSDEKDCTPRCDMDQFQCKSG C P CS E+SC +GRCI+ CDG DC DE + + C + CESGPHDVHKCSPREWSCPESGRCCISIYKVCDGILDCPGREDENNTSTGKYCSMTLCSAL	3623
Sbjct	256	CESGPHDVHKCSPREWSCPESGRCCISIYKVCDGILDCPGREDENNTSTGKYCSMTLCSAL	315
Query	3624	HC 3625	
Sbjct	316	NC 317	

Score = 159 bits (402), Expect = 1e-35
 Identities = 165/632 (26%), Positives = 240/632 (37%), Gaps = 109/632 (17%)

Query	3817	PGQPGCQDINECLRF-GTCSQLCENNKGHL---CSCARNFMKTHNTCKAEGSEYQVLVIA P P + N CL G CS LC G H C CA +++ A +E L A	3873
Sbjct	2335	PRSPADEVNNNCPLENNNGCSCSHLCFALPGLHTPKCDCAGFTLQSDGKNAISTE-NFLIFA	2393
Query	3874	DDNEIRSL-FPGPHPSAYEQAFQGDESFRVIDADMVHKAGRVYWTN---WHTGTISYRSL N +RSL HS Q + +V ++D +R+Y+T G ISY +L	3929
Sbjct	2394	LSNSLRSRLHLDPENHSPPFQINTVERTVM--SLDYDSVSDRIYFTQNLASVGQISYATL	2451
Query	3930	PAAAPPTTSNRHRRQIDRGVTHLNISGLKMPRGIAIDWVAGNVYWTDSGRDVIEVAQMKG T + SG+ GIA DW+ +Y+D +I G	3989
Sbjct	2452	SSGIHTPT-----VIASGIGTADGIAFDWITRRIYYSDYLNQMINSMaedg	2497
Query	3990	ENRKTLISGMIDEPAHIVVDPLRGTMWYSDWGNHNPKIETAAAMDGLTRELTVQDNIQWPTG NR + +P AIV+DP +G +YW+DW H KIE A + G R +V ++ P+G	4049
Sbjct	2498	SNRTVI--ARVPKPRAVLDCPCQGYLYWADWDTHAKIERATLGGNFRVPIVNSSLVMPMSG	2555
Query	4050	LAVDYHNERLYWADAKLSSVIGSIRLNGLDTPIVAAKDRKGLSHPFSIDVFPEDYIYGVTYIN LT+DYEDDLLYWVDASLQRIERSTLTVGDRREVIVNA--AVHAGLTLGYQQIYWTDLYT	4109
Sbjct	2556	LTLDYEDDLLYWVDASLQRIERSTLTVGDRREVIVNA--AVHAGLTLGYQQIYWTDLYT	2612
Query	4110	NRNFKIHKF-GHSPLVNLTTGGLSHASDVLYHQHKQPEVTPNPCRKK--CEWLCLLSPSG R+++ +K+ G + T LS + +++++ + NPC++ C +C P+G	4166
Sbjct	2613	QRIYRANKYDGSGQIAMTNLLSQPGRINTVVKNQKQCNCPCEQFNNGCSHICAPGPNG	2672
Query	4167	PVCTCPNGKRLDNGTCVPVPSPTPPPDAWRPGTCNLQCFNNGGSCFLNARRQPKCRCQPRY C CP+ N + R G + C NG RC	4226
Sbjct	2673	AECQCPCHE---GNWYLANNRKHICIVDNGERCGASSFTCSNG-----RCISEE	2716
Query	4227	TGDKCELDQCWEHCRNGGTCASPSGMPCTRCPTGFTGPKCTQQVCAGY---CANNSTC- KC+ D C +G S + TC PT FT C C Y C + C	4282

Blast Result

Sbjct	2717	W--KCDND---NDCGDGSDMESVCALHTC-SPTAFT---CANGRCVQYSYRCDDYNNDCG	2767
Query	4283	-TVNQNQNPQC---RCLP-GFLGD-----RCQYRQC-SGY- 4311 N + C RC+P F+ + C R C SGY	
Sbjct	2768	DGSDEAGCLFRDCNATTEFMCNNRRC1PREFICNGVDNCHDNNTSDEKNCPDRTCGSGYT	2827
Query	4312	-CENFGTC---QMAADGSQRQCRCRSTAYFEGSRCEVNKCS---RCLEGACVNVNKQSGDVTC 4363 C N C DG C + + C + CS +C G C+ D	
Sbjct	2828	KCHNSNICIPRVYLCDGNDCGDNSDENPTYCTTHTCSSLSEFQCASGRC1PQHWYCDQET	2887
Query	4364	NCTDGRVAP-----SCLTCVGHCNSNGSC 4387	
Sbjct	2888	+C D P +CL C +GG C DGGRC 2918	

Score = 153 bits (387), Expect = 5e-34
 Identities = 89/244 (36%), Positives = 119/244 (48%), Gaps = 28/244 (11%)

Query	2513	DDLTCRAVNSSCRAQDEFEC-ANGECAFNSLTCGVPHCKDKSDEKPSYCNSRRCKKTFR 2571 D++ C V +C+ Q F+C + G+CI S CD C D SDE+ C+ C
Sbjct	58	DEIGCAVV---TCQ-QGYFKCQSEGQCIPNSWVCDQDCDDGSDERQD-CSQSTCSSHQI 113
Query	2572	QCSNNGRCVSNMLWCNGADDGCGDGSDEIPCNKTAGCAGVGEFRCRDGTICGNSSRCNQFVDC 2631 CSNG+C+ + C+ DC DG+DE C C + C +G C S +C+ VDC
Sbjct	114	TCSNNGQCIPSEYRCDDHVRDCPDGADENDQCQYPTCE--QLTCDDNGACYNTSQKCDWKVDCR 171
Query	2632	DASDEMNCSATDCSSYFRLGVKGVLQFQPCERTSLCYAPSVCVDGANDCGDYSDERDCPGV 2691 D+SDE+NC+ + F G C +VCD NDC D SDE C
Sbjct	172	DSSDEINCTEICLNEFSCG-----NGECIPRAYVCDHDNDQDGDSDEHAC--- 217
Query	2692	KRPRCPLNYFACPCSGRCIPIMSWTCDEKEDCCEHGEDETHCNK-----FCSEAQFEC-QNH 2744 P C F CPSGRCI +W CD EDC+ DE C CS ++ C ++
Sbjct	218	NYPTCGGYQPTCPSPGRCIYQNWVCDGEDDCKDNGDEDGESGPHDVHKSPREWSCPESG 277
Query	2745	RCIS 2748
Sbjct	278	RCIS 281

Score = 122 bits (305), Expect = 2e-24
 Identities = 99/276 (35%), Positives = 128/276 (46%), Gaps = 29/276 (10%)

Query	801	QVGTNKRVRNNGCCSLLATPGSRQCACAEQVLADGVTLANPSYVPPPPQCPGEFA 860 Q G KC+ + G C + C D+ D TC ++ QC P E+ Sbjct 68 QQYFKCQ-SEGQCIPNSWVCDQDCDDGSDERQDCSQTCSHHQITCSNGQCIPSEY-
Query	861	CANSRCTQERWKCDGNDCLDNDEAPALCHQHTCPSDRFKCENNRCIPNRWLCDGDNDC 920 +CD DC +DE C TC ++ C+N C CD DC Sbjct 126 -----RCDHVRDCPDGAEND--CQYPTC-EQLTCDDNGACYNTSQKCDWKVDC 170
Query	921	GNSEDESNATCSARTCPNNQFSCASGRC1PISWTCDLDDCGDRSDESASCAYPTCPPLT 980 +S DE N T C N+FSC +G CIP ++ CD D SDE A C YPTC Sbjct 171 RDSSDEINCT---EICLNEFSCGNCECIPRAYVCDHDNDQDGDSDEHA-CNYPTCGGY- 225

Blast Result

Query 981	QFTCNNNGRCININWRCDDNDDCGDNNSDEAGCS-----	HSCSSTQFKC-NSGRCIPEHWT	1033
	QFTC +GRCI NW CD ++DC DN DE GC H CS ++ C SGRCI +		
Sbjct 226	QFTCPGSGRCIYQNWNVCDGEDDCKDNGDEDGCESGPHDVHKCSPREWSCPESGRCISIYKV		285
Query 1034	CDGDNDCCGDYSDETHANCTNQATRPPGGCHTDEFQC	1069	
	CDG DC DE + + + +QC		
Sbjct 286	CDGILDCCPGREDENNTSTGKYCSMTLCSALNCQYQC	321	



Score = 119 bits (298), Expect = 1e-23

Identities = 117/488 (23%), Positives = 191/488 (39%), Gaps = 66/488 (13%)

Query 3963	IAIDWVAGNVYWTDSGRDVRIVEVAQMKGRENKTLISGMIDEPAHAIVVDPRLRGTMWSDWGN	4022
	+A DW++ N+WTDS I V ++ + R+T++ ++ P ++V V P G ++++DW	
Sbjct 789	LAFDWISKNLWYTDSHYKSISVMRLADKTRRTVVQ-YLNNPRSVVVHPFAGYLFFTDWFR	847
Query 4023	HPKIELTAAAMDGLTRELTVQDNIQWPTGLAVDYHNERLYWADAKLSVIGSIRNLNGTDPIVA	4082
	KI A DG+ ++ + WP GLA+D+ RLYW DA I +G D	
Sbjct 848	PAKIMRAWSGDGHLLPVINTTLGWPNGLAIWDWAASRLYLVWDAYFDKIEHSTFDGLDRRRRL	907
Query 4083	ADSKRGLSHPPSIDVFDYIYGVTYINNRVFIKHFSPPLVNLTGLSHASDVVLYHQH	4142
	++ ++HPF + +F ++++ + + ++ K + + G+++ + Y +	
Sbjct 908	GHIEQ-TMHPFGLAIFGEHLFFTDWRLGAIIRVRKADGEMTVIRSGIAYILHLKSYDVN	966
Query 4143	KQPEVTNTPCDRK-----KCEWLCLLSPS-GPVCTCPNGKRLDNGTCVPVPSPTPPPDAPR	4196
	Q +N C++ C C P+ VC CP G RL + PT P +	
Sbjct 967	IQTG-SNACNQPPTHNGDCSHFCFPVNQFQRVCVGCPYGMRLASNLTCEDGPTNEPTEQ	1025
Query 4197	PGTCNLQCFNGGSCFLNARRQPKCRCQPYRTGDKCE-LDQWHEHCRN-----GGTCAAS	4249
	G + C NG RC P Y C+ +D C ++ TC++S	
Sbjct 1026	CGLFSFPCKNG-----RCVPNYY---LCDGVDDCHDNSDEQLCGTLNNTCSSS	1070
Query 4250	--PSGMPTC-----RCPTGFTGPCKTQQVCAGYCANNSTCTVNQGNQPQCRC-L	4295
	G C C G C A TC +Q C	
Sbjct 1071	AFTCGHGECPAPIAHWRCDKRNDCVDGSDEHNCPTHAPASCLDTQYTCDNHQCLSKNWVCDT	1130
Query 4296	PGFLGDRQCYRQCSGYCENFGTCQMAADGSRQCRCTAYFEGSRCEVNKCSRCLEGA----	4351
	GD + C+ + TCQ + RC C+ +K C++G+	
Sbjct 1131	DNDCGDGDSDEKNCN---STETCQPSQFNCPNHRICDL--SFVCDGDK--DCVDGDSDEVG	1182
Query 4352	CVNWKQSGDVTNCNTDGRVAPSCLTIVGHCNSNGSCTMNSKMMPECQCPPHMTGPRCEEH	4411
	CV+N + C D C+ C + NS E CP G C	
Sbjct 1183	CVLNCTASQFKCASGD-----KCIGVTNRCGVFDCSDNS--DEAGCPTRPPG-MCHSD	1233
Query 4412	VFSQQQPG 4419	
	F Q+ G	
Sbjct 1234	EFQCQEDG 1241	



Score = 104 bits (259), Expect = 4e-19

Identities = 61/180 (33%), Positives = 84/180 (46%), Gaps = 21/180 (11%)

Query 3297	NNGGCSNLCLLSPGGGHKCACPTNFYLGSDGRTCVSNCTASQFVCKNDKCIIPFWWKCDTE	3356
	+NG C N KC + SD C C ++F C N +CIP + CD +	

Blast Result

Sbjct	153	DNGACYNT-----SQKCDWKVDCRDSSDEINC TEI CLHNEFSCGN GEC I PRAY VCDHD	205
Query	3357	DDCGDHSDEPPDCPEFKCRPGQFCSTGICTNPFAICDGDNDQDQNSDEANC----DIH +DC D SDE C C QF C +G C ++CDG++DC+DN DE C D+H	3411
Sbjct	206	NDCQDGSDDEHA-CNYPTCGGYQFTCPSPGR CIYQN WVC DGEDDCKDNGDEDGCESGP HDVH	264
Query	3412	VCLPSQFKCTNTNRCI P G I FRCNGQDN CGD EDERD----CPEVTCAP--NQF QCSIT C P ++ C + RCI C+G EDE + C C+ Q+QC T	3463
Sbjct	265	KCSPREWSCPESGRCISIYKVCDGILDCPGR EDENN NTSTGKYCSMTLCSALNCQYQCHET	324



Score = 94.0 bits (232), Expect = 5e-16

Identities = 75/261 (28%), Positives = 98/261 (37%), Gaps = 36/261 (13%)

Query	2490	QDLCLLTHQGHVNCSRCRRGILQDDLTCA RVNSSCRAQDEF ECA-----NGECIN	2539
	OD	T H + C G+ + C V DE + C NG C N	
Sbjct	101	QDCSQTCSHH-QITCSNQOCIPSEYRCDHV RDCPDGA DENDCQYPTCEQLTCDNGACYN	159
Query	2540	FSLTCGVPHCKDKSDEKPSYCNSRRCKTFROCSNGRCVS NMLWCNGADDCGDGSDEIP	2599
	S CD	C+D SDE + C C NG C+ C+ +DC DGSDE	
Sbjct	160	TSQKCDWV KCDR DSSDE INC---TEI CLHNEFSCGN GEC I PRAY VCDHD NDCD QDGSDE HA	216
Query	2600	CNKTAGVGEFRCRDGT CIGNSSRCNQFVD CEDAS DEM NC SAT DCSSYFRLGVKGVL FQP	2659
	CN	CG + F C G CI + C+ DC+D DE C S +	
Sbjct	217	CNYPTCGGYQFTCPSPGR CIYQN WVC DGEDDCKDNGDEDGCE---SGPHDVHKCSPREWS	272
Query	2660	CERTS LCYAPS W VCDG AND CGD Y S D E R D C P G V K -----RPRCPL NYFA---C	2703
	C + C +	VC DG DC DE + K + + C + C	
Sbjct	273	CPESGRCISIYKVCDGILDCPGR EDENN NTSTGKYCSMTLCSALNCQYQCHETPYGGACFC	332
Query	2704	PSGRCI PM--SWTCDKEDDCE	2722
	P G I	S TC + DDC+	
Sbjct	333	PPGYI INH NDS RT C VEF FDCQ	353



Score = 78.6 bits (192), Expect = 2e-11

Identities = 46/109 (42%), Positives = 57/109 (52%), Gaps = 10/109 (9%)

Query	23	APKTCSPKQFACRQD QITCISK GWRCDGERDCP DGSDE APEI CPQSKAQR CQP -NEH NCLG	81
	A +TC P QF C +	CI + W+CD + DC D SDE E C S A C E +C	
Sbjct	3631	ASRTCRPQQFRCANG-R CIP QAWKCDV DND CGDH SDEPI EEC-MSSAHLCDNFTEFSCKT	3688
Query	82	TEL CVPMSRLCNGVQDCMDGSDEGPHCRELQGNCSRLG---CQ-HHC VP	126
	C+P	+CNGV DC D SDE C E C +G C+ HHC+P	
Sbjct	3689	NYRCIPKWA VCN GVD DCR D NSDE-QGCEE --RTCHPVGFDRCKNHH CIP	3734



Score = 78.2 bits (191), Expect = 3e-11

Identities = 93/430 (21%), Positives = 162/430 (37%), Gaps = 72/430 (16%)

Query 25	KTCSPKQFACRDQITCISKWRCRDGERDCPDGSDEAPEICPQSKAQRCQPNEHNCLGTE-	83
	+TC +F C D CI W CDG+ DC D SDE Q + Q C +E C+	
Sbjct 2904	RTCLADEFKC-DGGRCIPSEWICDGDNDGCDMSDEDKR--HQCNQNCSDSEFLCVNDRP	2960
Query 84	---LCVPMRSRLCNGVQDCMDGSDEGPCHCRELQGNCSRLGCQHH-CVPTLDGPTCYCNSSF	139
	C+P S +C+G DC DG DE +C + + C + C+P + C ++	
Sbjct 2961	PDRRCIPQSWSVCDGVDCTDGYDENQNCTRRTCSENEFTCGYGLCIPKIF--RCDRHND	3018
Query 140	QLQADGKTCDFDECSVYGTCSQ---LCTN---TDGSFIC---GCVEG----YLLQPD	184
	+D + C +Y TC Q C N +F+C C +G +L	
Sbjct 3019	GDYSDERGC-----LYQTCCQONQFTCQNGRCISKTFCVCDENDCDCGDSDELMHLCHTP	3071
Query 185	NRSCKAKNEPVDRPPVLLIANQNLATLTYLSGAQVSTITPTSTRQTTAMFSYANETVCW	244
	+C D + + N L L + + + +	
Sbjct 3072	EPTCPPHEFKCDNGRCIEMMKLKNHLDLDCDNSDEKGCGINECH-----DPSISG	3121
Query 245	VHVGSAAQTQLKCARMPGLKGFVDEHT---INISLSLHHVQEQAIDWLTGNFY-----	295
	+ T C+ PG K D+ T I+ + V + + G++	
Sbjct 3122	CDHNCTDTLTSFYCSCRPGYKLMSDKRTCVDIDECTEMPFVCSQKCENVIGSYICKAPG	3181
Query 296	FVDDIDDRIFVCNRNGDTCTVTLDDLELYNPKGIALD-----PAMGKVFFTDYQIPIK	347
	++ + D + C +N + L + Y + + + D + + V + + G++	
Sbjct 3182	YLREPDKT--TCRQNSNIEPYLIFSNRYLRLNTIDGYFYSLILEGLDNVVALDFDRVEK	3239
Query 348	-----VERCDMDGQNRTKLVDKSVKIVFPHGITLDLVSRLVWADAYLDYIEVVVDY	396
	+ER + + N+ + + + + + D VSR +W DA LD + V D	
Sbjct 3240	RLYWIDTQRQVIERMFLNKTNKETIIHRLPAAESLAVDWVSRKLYWLDARLDGLFVSDL	3299
Query 397	EGKGGRQTIQ 406	
	G R+ + Q	
Sbjct 3300	NGGHRRMLAQ 3309	



Score = 73.2 bits (178), Expect = 9e-10
 Identities = 44/139 (31%), Positives = 63/139 (45%), Gaps = 26/139 (18%)

Query 22	DAPKTCSPKQFACRDQITCISKWRCRDGERDCPDGSDEAPEICPQSKAQRCQPNEHNCLG	81
	++ +TC P QF C + CI + CDG+ +DC DGSDE + C ++ C	
Sbjct 1144	NSTETCPQSFNCNPNH-RCIDLSPVCDGDKDCVCDGSDEVGCVL-----NCTASQFKCAS	1196
Query 82	TELCVPMSRLCNGVQDCMDGSDEGPCHCRELQGNCSRLGCQHHCVPTLDGPTCYCNSSF	141
	+ C+ + C+G DC D SDE GC PT C+ + FQ	
Sbjct 1197	GDKCIGVTNRCDGVFDCCSDNSDEA-----GC-----PTRPPGMCH-SDEFQ	1237
Query 142	QADGKTCDFDECSVYGT C 160	
	Q DG +F EC + C	
Sbjct 1238	QEDGICIPNFWECGDGH PDC 1256	



Score = 72.8 bits (177), Expect = 1e-09
 Identities = 54/170 (31%), Positives = 77/170 (45%), Gaps = 39/170 (22%)

Query 26	TCSPKQFACRDQITCISKWRCRDGERDCPDGSDEAPEICPQSKAQRCQPNEHNCLGTEL	85
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Blast Result

Sbjct	66	TC F C + CI W CD ++DC DGSDE + C QS C ++ C + C TCQQQYFKCQSEGQCIPNSWVCDQDQDCDDGSDERQD-CSQS--TCSSHQITCSNGQ-C	120
Query	86	VPMRSRLCNGVQDCMDGSDEG---PHCRELQGNCSRLGCQHHCVPTLDGPTCYCNSSFQL	141
		+P C+ V+DC DG+DE P C +L T D CY S	
Sbjct	121	IPSEYRCRDHVRDCPDGADENDQCYPTECEQL-----TCDNGACYNTSQ---	162
Query	142	QADGKT-CKD-FDECSVYGTCSQLCTNTDGSFIGC---CV-EGYLLQPDN 185 + D K C+D DE + C++C + + F CG C+ Y+ DN	
Sbjct	163	KCDWKVDCRDSSDEIN---CTEICLHNE--FSCGNGEC1PRAYVCDHDN 206	



Score = 69.7 bits (169), Expect = 1e-08
 Identities = 52/165 (31%), Positives = 69/165 (41%), Gaps = 20/165 (12%)

Query	21	IDAPKTCSPKQFACRQITCISKGWRCDGERDCPDGSDEAPEICPQSKAQRQCOPNEHNCL 80 +D + C F C + CIS+ W+CD + DC DGSDE +C C P C	
Sbjct	2694	VDNGERCGASSFTCSNG-RCISEEWKCDNDNDCGDSDEMESVC---ALHTCSPTAFTCA	2749
Query	81	GTELCVPMSRLCNGVQDCMDGSDE-GPHCRELQGNCSRLGCQHHCVP---TLDG-PTCYC 135 CV S C+ DC DGSDE G R+ + C+P +G C+	
Sbjct	2750	NGR-CVQYSYRCDDYYNDCGDSDEAGCLFRDCNATTEFCMNRRCIPREFICNGVNDCHD 2808	
Query	136	NSSFQLQADGKTCDFDECSVYGTC--SQLCTN---TDGSFIGC 174 N++ +D K C D S Y C S +C DG CG	
Sbjct	2809	NNT---SDEKNCPDRTCQSGYTKCHNSNICIPRVYLCDGDNDCG 2849	



Score = 64.7 bits (156), Expect = 3e-07
 Identities = 44/149 (29%), Positives = 60/149 (40%), Gaps = 13/149 (8%)

Query	25	KTCSPKOFACRQITCISKGWRCDGERDCPDGSDEAPEICPQSKAQRQCOPNEHNCLTEL 84 +TC C + CI + + CDG+ DC D SDE P C C + E C +	
Sbjct	2820	RTCQSGYTKCHNSNICIPRVYLCDGDNDCGDNSDENPTYC---TTHTCSSSEFQC-ASGR 2875	
Query	85	CVPMSRLCNGVQDCMDGSDEGPHCRELQGNCSRLGCQHHCVPTLDGPTCYCNSSFQLQAD 144 C+P C+ DC D SDE C + C L + C DG C S + D	
Sbjct	2876	CIPQHWYCDQETDCFASDEPASCGBHERTC--LADEFKC---DGGRC-IPSEWICDGD 2928	
Query	145	GKTCKDFDECSVYGTCSQLCTNTDGSFIGC 173 DE + +Q C +D F+C	
Sbjct	2929	NDCGDMDEDKRHQCONQNC--SDSEFLC 2955	



Score = 60.8 bits (146), Expect = 5e-06
 Identities = 36/113 (31%), Positives = 47/113 (41%), Gaps = 20/113 (17%)

Query	23	APKTCSPKQFACRQITCISKGWRCDGERDCPDGSDEAPEICPQSKAQRQCOPNEHNCLGT 82 AP+ C+ +F C +Q CI W CD DC D SDE + + C P C	
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Blast Result

Sbjct 3755 APRECTESEFRCVNQ-QCIPSRWICDHYNDCGDNSDER-----DCEMRTCHPEYFQCTSG 3808
Query 83 ELCVPMSRLCNGVQDCMDGSDE-----GPHCRELQGNCSRLGCQHHCVP I26
CV C+G DC+D SDE G +C+ C H C+P
Sbjct 3809 H-CVHSELKCDGSADCLDASDEADCPTRFPDGAYCQATMFECK---NHVCIP 3856

Score = 57.8 bits (I38), Expect = 4e-05
Identities = 31/81 (38%), Positives = 43/81 (53%), Gaps = 8/81 (9%)

Query 25 KTCSPK-QFACRDOITCISKGWRCDGERDCPDGSDEAPEICPQSKAQRQCQPNEHNCLGTE 83
+TC P F C++ CI W+CDG+ DC D SDE E C + C +E C+ +
Sbjct 3717 RTCHPVGDFRCKNH-HCIPLRWQCDGQNDCGDNSD--ENC---APRECTESEFRCVNQQ 3770

Query 84 LCVPMSRLCNGVQDCMDGSDE 104
C+P +C+ DC D SDE
Sbjct 3771 -CIPSRWICDHYNDCGDNSD 3790

CPU time: 0.08 user secs. 0.05 sys. secs 0.13 total secs.